

AMENDMENTS TO THE CLAIMS:

This listing of the claims will replace all prior listings and versions of claims in the application.

CLAIMS

1. (currently amended) A method of identifying individuals having a polymorphism, comprising;
 - a. providing nucleic acid from a subject; and
 - b. detecting the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID NOS: 7063, 7064, ~~7071~~ 7070, 7073, and 7074, wherein in SEQ ID NO: 7063, said polymorphism is designated by an r, wherein r is a g or an a, wherein in SEQ ID NO: 7064 said polymorphism is designated by an s, wherein in SEQ ID NO: 7070, said polymorphism is designated by an n, wherein n is a t or a deletion, wherein in SEQ ID NO 7073 said polymorphism is designated by an n, wherein said n is an a or a deletion, and wherein in SEQ ID NO: 7074 said polymorphism is designated by an n, wherein said n is an a or a deletion.
- 2-4. (canceled)
5. (original) The method of Claim 1, wherein said detecting step comprises use of a hybridization assay.
6. (original) The method of Claim 1, wherein said detecting step comprises use of a TAQMAN assay.
7. (original) The method of Claim 1, wherein said detecting step comprises use of an invasive cleavage assay.

8. (original) The method of Claim 1, wherein said detecting step comprises use of mass spectroscopy.

9. (original) The method of Claim 1, wherein said detecting step comprises use of a microarray.

10. (original) The method of Claim 1, wherein said detecting step comprises use of a polymerase chain reaction.

11. (original) The method of Claim 1, wherein said detecting step comprises use of a rolling circle extension assay.

12. (original) The method of Claim 1, wherein said detecting step comprises use of a sequencing assay.

13. (original) The method of Claim 1, wherein said detecting step comprises use of a hybridization assay employing a probe complementary to a polymorphism.

14. (original) The method of Claim 1, wherein said detecting step comprises use of a bead array assay.

15. (original) The method of Claim 1, wherein said detecting step comprises use of a primer extension assay.

16. (original) The method of Claim 1, wherein said detecting step comprises use of an enzyme mismatch cleavage assay.

17. (original) The method of Claim 1, wherein said detecting step comprises use of a branched hybridization assay.

18. (original) The method of Claim 1, wherein said detecting step comprises use of a NASBA assay.

19. (original) The method of Claim 1, wherein said detecting step comprises use of a molecular beacon assay.

20. (original) The method of Claim 1, wherein said detecting step comprises use of a cycling probe assay.

21. (original) The method of Claim 1, wherein said detecting step comprises use of a ligase chain reaction assay.

22. (original) The method of Claim 1, wherein said detection step comprises use of a sandwich hybridization assay.

23-36. (canceled)

37. (currently amended) A method for screening subjects for genetic markers associated with drug metabolizing enzyme(s), comprising:

- a) providing a biological sample comprising a nucleic acid from a subject;
- b) testing said nucleic acid for a polymorphism in a genetic marker associated with a drug metabolizing enzyme, said genetic marker comprising one or more nucleotide polymorphisms ~~designated by n, said n selected from a base substitution, an insertion, or a deletion found in a sequence~~ selected from the group consisting of polymorphisms in SEQ ID Nos: 7063, 7064, ~~7071~~ 7070, 7073, and 7074, wherein in SEQ ID NO: 7063, said polymorphism is designated by an r, wherein r is a g or an a, wherein in SEQ ID NO: 7064 said polymorphism is designated by an s, wherein in SEQ ID NO: 7070, said polymorphism is designated by an n,

wherein n is a t or a deletion, wherein in SEQ ID NO 7073 said polymorphism is designated by an n, wherein said n is an a or a deletion, and wherein in SEQ ID NO: 7074 said polymorphism is designated by an n, wherein said n is an a or a deletion.

38. (original) The method of Claim 37, wherein said biological sample is selected from the group consisting of blood, saliva, amniotic fluid, and tissue.

39. (original) The method of Claim 37, wherein said subject is a human.

40. (original) The method of Claim 37, wherein said nucleic acid comprises DNA.

41. (original) The method of Claim 37, wherein said nucleic acid comprises RNA.

42-75. (canceled)

76. (currently amended) A The method of ~~prescribing a drug to or treatment protocol for a subject, comprising;~~

- a. ~~providing nucleic acid from said subject;~~
- b. ~~Claim 37, wherein said testing comprises using a detection assay to detect the presence of at least one said one or more polymorphisms in said genetic marker nucleic acid, said at least one polymorphism selected from the group consisting of said polymorphisms found in SEQ ID Nos: 7063, 7064, 7071, 7073, and 7074; and,~~
- c. ~~prescribing said drug or treatment protocol based upon the result of said detection assay.~~

77-79 (canceled)

80. (original) The method of Claim 76, wherein said detection assay comprises a hybridization assay.

81. (original) The method of Claim 76, wherein said detection assay comprises a TAQMAN assay.

82. (original) The method of Claim 76, wherein said detection assay comprises an invasive cleavage assay.

83. (original) The method of Claim 76, wherein said detection assay comprises mass spectroscopy.

84. (original) The method of Claim 76, wherein said detection assay comprises a microarray.

85. (original) The method of Claim 76, wherein said detection assay comprises a polymerase chain reaction.

86. (original) The method of Claim 76, wherein said detection assay comprises a rolling circle extension assay.

87. (original) The method of Claim 76, wherein said detection assay comprises a sequencing assay.

88. (original) The method of Claim 76, wherein said detection assay comprises a hybridization assay employing a probe complementary to a polymorphism.

89. (original) The method of Claim 76, wherein said detection assay comprises a bead array assay.

90. (original) The method of Claim 76, wherein said detection assay comprises a primer extension assay.

91. (original) The method of Claim 76, wherein said detection assay comprises an enzyme mismatch cleavage assay.

92. (original) The method of Claim 76, wherein said detection assay comprises a branched hybridization assay.

93. (original) The method of Claim 76, wherein said detection assay comprises a NASBA assay.

94. (original) The method of Claim 76, wherein said detection assay comprises a molecular beacon assay.

95. (original) The method of Claim 76, wherein said detection assay comprises a cycling probe assay.

96. (original) The method of Claim 76, wherein said detection assay comprises a ligase chain reaction assay.

97. (original) The method of Claim 76, wherein said detection step comprises a sandwich hybridization assay.

98. (currently amended) The method of Claim 76, in which said detection assay comprises a kit for detecting a polymorphism, said kit comprising at least one reagent that specifically detects a at least one of said one or more polymorphisms in said genetic marker~~in a sequence selected from the group consisting of SEQ ID Nos: 7063, 7064, 7071, 7073, and 7074 designated by n in a sequence selected from SEQ ID Nos: 7063, 7064, 7071 7070, 7073, and 7074, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.~~

99. (currently amended) The method of Claim 98, further comprising instructions for ~~determining whether the subject is at increased risk of having a drug metabolism disorder~~ screening subjects for genetic markers associated with drug metabolizing enzyme(s).

100. (original) The method of Claim 99 98, wherein said at least one reagent comprises a nucleic acid probe.

101. (original) The method of Claim 98, wherein said kit comprises an in vitro diagnostic detection assay.

102. (original) The method of Claim 98, wherein said kit comprises an analyte specific reagent detection assay.

103. (original) The method of Claim 98, wherein said kit comprises a research-use-only detection assay.

104. (original) The method of Claim 76, wherein said nucleic acid is obtained from a biological sample, said sample being selected from the group consisting of blood, saliva, amniotic fluid, and tissue.

105. (original) The method of Claim 104, wherein said subject is a human.

106. (original) The method of Claim 104, wherein said nucleic acid comprises DNA.

107. (original) The method of Claim 104, wherein said nucleic acid comprises RNA.

108. (original) The method of Claim 104, wherein said kit comprises PCR primers.

109. (previously presented) The method of claim 98, in which said kit comprises an array of detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting at least one of said one or more nucleotide polymorphisms in said genetic marker designated by n in SEQ ID Nos: 7063, 7064, 7071, 7070, 7073, and 7074, wherein n represents a base substitution, insertion, or deletion compared to a wild type sequence.

110. (original) The method of Claim 109, wherein said detection assay is selected from the group consisting of a sequencing assay, a polymerase chain reaction assay, a hybridization assay, a hybridization assay employing a probe complementary to a polymorphism, a microarray assay, a bead array assay, a primer extension assay, an enzyme mismatch cleavage assay, a branched hybridization assay, a rolling circle replication assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

111-123. (canceled)